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OM protein - protein search, using sw model

Run on: October 28, 2003, 08:57:32 ; Search time 28 Seconds
(without alignments)
10.578 Million cell updates/sec

Title: US-09-847-940b-6

Perfect score: 7

Sequence: 1 XXXXXX 7

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/2/1aa/5A_COMB_depp:
2: /cgn2_6/prodata/2/1aa/5B_COMB_depp:
3: /cgn2_6/prodata/2/1aa/6A_COMB_depp:
4: /cgn2_6/prodata/2/1aa/6B_COMB_depp:
5: /cgn2_6/prodata/2/1aa/PCTMUS_COMB_depp:
6: /cgn2_6/prodata/2/1aa/backfile1_depp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100	0	7 1 US-07-700-526-17	Sequence 17, Appl
2	7	100	0	7 1 US-07-690-284A-8	Sequence 8, Appl
3	7	100	0	7 1 US-07-690-284A-12	Sequence 21, Appl
4	7	100	0	7 1 US-07-720-222-21	Sequence 2, Appl
5	7	100	0	7 1 US-07-855-793-2	Sequence 6, Appl
6	7	100	0	7 1 US-07-866-678-2	Sequence 10, Appl
7	7	100	0	7 1 US-07-866-678-6	Sequence 12, Appl
8	7	100	0	7 1 US-07-866-678-10	Sequence 11, Appl
9	7	100	0	7 1 US-07-670-296-5	Sequence 51, Appl
10	7	100	0	7 1 US-07-670-296-12	Sequence 4, Appl
11	7	100	0	7 1 US-07-689-933B-17	Sequence 25, Appl
12	7	100	0	7 1 US-07-12-628B-7	Sequence 26, Appl
13	7	100	0	7 1 US-07-63-113-20	Sequence 28, Appl
14	7	100	0	7 1 US-07-63-413-25	Sequence 53, Appl
15	7	100	0	7 1 US-07-596-867C-8	Sequence 1, Appl
16	7	100	0	7 1 US-07-657-769B-11	Sequence 51, Appl
17	7	100	0	7 1 US-07-657-769B-51	Sequence 4, Appl
18	7	100	0	7 1 US-07-935-310A-4	Sequence 25, Appl
19	7	100	0	7 1 US-07-78-233B-25	Sequence 26, Appl
20	7	100	0	7 1 US-07-718-774A-26	Sequence 28, Appl
21	7	100	0	7 1 US-07-718-274A-28	Sequence 51, Appl
22	7	100	0	7 1 US-07-718-774A-51	Sequence 63, Appl
23	7	100	0	7 1 US-07-718-274A-63	Sequence 2, Appl
24	7	100	0	7 1 US-07-715-650-2	Sequence 5, Appl
25	7	100	0	7 1 US-07-830-330-5	Sequence 7, Appl
26	7	100	0	7 1 US-07-626-923A-7	Sequence 1, Appl
27	7	100	0	7 1 US-07-883-491-1	

ALIGNMENTS

RESULT 1
US-07-700-526-17
Sequence 17, Application US/07700526
Patent No. 516613
GENERAL INFORMATION:
APPLICANT: Houston, L. L.
Liu, David Y.
Kaymalkhan, Zehra
TITLE OF INVENTION: Method for Inhibiting Adhesion of White Blood Cells to Endothelial Cells
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-Third Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/700,526
FILING DATE: 19910316
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Phillip L.
REGISTRATION NUMBER: 31,395
REFERENCE DOCKET NUMBER: 2600.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 420-3217
TELEFAX: (415) 658-5239
TELEX: 4922659
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-07-700-526-17

Query Match Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7 :::::::

RESULT 2
US-07-690-284A-8
; Sequence 8, Application US/07690284A
; Patent No. 517253
; GENERAL INFORMATION:
; APPLICANT: Fallon, Robert J.
; COMPUTER: Bullock, Joseph W.
; APPLICANT: Adams, Steven P.
; APPLICANT: Perlmutter, David H.
; TITLE OF INVENTION: Inhibitory Peptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Bldg A3SD
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/690,284A
; FILING DATE: 19910424
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25275
; REFERENCE/DOCKET NUMBER: 07-24 (760) A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 694-3117
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-690-284A-8

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0;
Gaps 0;

RESULT 4
US-07-720-222-21
; Sequence 21, Application US/07720222
; Patent No. 5190873
; GENERAL INFORMATION:
; APPLICANT: Lehrhardt, Waldemar
; COMPUTER: Bourdon, Mario
; APPLICANT: Youderian, Phil
; TITLE OF INVENTION: HYBRID PROTEINS CONTAINING BINDING SITES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bingham & Pitting
; STREET: 11230 Sorrento Valley Road, Suite 200
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 19910621
; FILING DATE: 19910621
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bingham, Douglas A.
; REGISTRATION NUMBER: 32,457
; REFERENCE/DOCKET NUMBER: C1B0012P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-587-3533
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear

RESULT 3
US-07-690-284A-12
; Sequence 12, Application US/07690284A
; Patent No. 517253
; GENERAL INFORMATION:
; APPLICANT: Fallon, Robert J.
; COMPUTER: Bullock, Joseph W.
; APPLICANT: Adams, Steven P.
; APPLICANT: Perlmutter, David H.
; TITLE OF INVENTION: Inhibitory Peptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Bldg A3SD
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:

MOLECULE TYPE: peptide

US-07-720-222-21

Query Match 100.0%; Score 7; DB 1; Length 7;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 7; Mismatches 0; Gaps 0;

Indels 0;

Qy 1 XXXXXX 7

Db 1 SRRGDM 7

RESULT 5

; Sequence 2, Application US/07855793

; Patent No. 5217880

; GENERAL INFORMATION:

; APPLICANT: Massanori MITTA et al.

; TITLE OF INVENTION: L-FUCOSE DEHYDROGENASE GENE, MICROORGANISM HAVING SAID GENE AND PRODUCTION OF L-FUCOSE

; TITLE OF INVENTION: DEHYDROGENASE BY THE USE OF SAID MICROORGANISM

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: DisplayWrite

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/855,793

; FILING DATE: 19920323

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX:

; TELEX:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acid residues

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Peptide

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE: internal fragment

; ORIGINAL SOURCE:

; ORGANISM: Arthrobacter Oxidans

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE:

; CELL LINE:

; ORGANELLE:

; IMMEDIATE SOURCE:

; LIBRARY:

; CLONE:

; POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

US-07-855,793-2

RELEVANT RESIDUES IN SEQ ID NO:

Query Match 100.0%; Score 7; DB 1; Length 7;

Best Local Similarity 0.0%; Pred. No. 0;

Mismatches 0; Conservative 7; Gaps 0;

Indels 0;

Qy 1 XXXXXX 7

Db 1 WGAQM 7

RESULT 6

US-07-866-678-2

; Sequence 2, Application US/07866678

; Patent No. 5225531

; GENERAL INFORMATION:

; APPLICANT: Gresham, Hattie D.

; APPLICANT: Brown, Eric J.

; APPLICANT: Adams, Steven P.

; TITLE OF INVENTION: No. 5225531el Hexapeptide

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG

; STREET: 800 N. Lindbergh

; CITY: St. Louis

; STATE: Missouri

; COUNTRY: USA

; ZIP: 63167

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/866,678

FILING DATE: 19920409

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Meyer, Scott J.

REGISTRATION NUMBER: 25,275

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 694-3117

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acid residues

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE: internal fragment

ORIGINAL SOURCE:

ORGANISM: Arthrobacter Oxidans

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

Query Match 100.0%; Score 7; DB 1; Length 7;

Best Local Similarity 0.0%; Pred. No. 0;

US-07-866-678-2

Query Match 100.0%; Score 7; DB 1; Length 7;

Best Local Similarity 0.0%; Pred. No. 0;

RESULT 7
US-07-866-678-6
Sequence 6, Application US/07866678
Patent No. 522551
GENERAL INFORMATION:
APPLICANT: Gresham, Hattie D.
APPLICANT: Brown, Eric J.
APPLICANT: Adams, Steven P.
TITLE OF INVENTION: No. 5225531el Hexapeptide
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/866-678
FILING DATE: 19920409
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-24 (867) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-866-678-10

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0;
Gaps 0;

RESULT 8
US-07-866-678-10
Sequence 10, Application US/07866678
Patent No. 5225531
GENERAL INFORMATION:
APPLICANT: Gresham, Hattie D.
APPLICANT: Brown, Eric J.
APPLICANT: Adams, Steven P.
TITLE OF INVENTION: No. 5225531el Hexapeptide
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0;
Gaps 0;

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0;
Gaps 0;

RESULT 9
US-07-670-296-5
Sequence 5, Application US/07670296
Patent No. 522964
GENERAL INFORMATION:
APPLICANT: Ohiodi, Francesca
TITLE OF INVENTION: POLYPEPTIDES DERIVED FROM THE HUMAN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & Milnamow
STREET: 11300 Sorrento Valley Road, Suite 200
CITY: San Diego
STATE: CA
COUNTRY: U.S.A.
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/670,296
FILING DATE: 19910607
CLASSIFICATION: 530
PRIMER APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Birmingham, Douglas A.
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: BCI-0009P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-5555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal

FEATURE:
 NAME/KEY: Region
 LOCATION: 1-7
 OTHER INFORMATION: /note= "An amino terminal group representing amino acid residue "Xaa" at position
 OTHER INFORMATION: #1, in Sequence I.D. #1."
 US-07-670-296-5

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db ::::: 7
 GYIEAEV 7

RESULT 10
 US-07-670-296-12
 Sequence 12, Application US/07670296
 GENERAL INFORMATION:
 Patent No. 5229364

APPLICANT: Chiodi, Francesca
 TITLE OF INVENTION: POLYPEPTIDES DERIVED FROM THE HUMAN IMMUNODEFICIENCY VIRUS ENDONUCLEASE PROTEIN
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & Milmanow
 STREET: 11300 Sorrento Valley Road, Suite 200
 CITY: San Diego
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92121

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOSS/MS-DOS
 SOFTWARE: Parent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/670,296
 FILING DATE: 19910607
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Birmingham, Douglas A.
 REGISTRATION NUMBER: 32,457
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-546-1555
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: C-terminal
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1-7
 OTHER INFORMATION: /note= "A carboxy terminal group representing amino acid residue "Xaa" at position
 OTHER INFORMATION: #22, in Sequence I.D. #1."
 US-07-670-296-12

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db ::::: 7
 TIRTDNG 7

RESULT 11
 US-07-689-693B-17
 Sequence 17, Application US/07689693B
 Patent No. 5221011
 GENERAL INFORMATION:
 APPLICANT: David Hilliard
 APPLICANT: Baldomero M. Olivarra
 TITLE OF INVENTION: Segregated Folding Determinants
 TITLE OF INVENTION: for Small Disulfide-Rich Peptides
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Thorpe, No. 5231011th & Western
 STREET: 9035 South 700 East, Suite 200
 CITY: Sandy
 STATE: Utah
 COUNTRY: USA
 ZIP: 84070
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
 COMPUTER: Compaq LTE/286
 OPERATING SYSTEM: DOS 4.01
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/689,693B
 FILING DATE: 19910418
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: none
 FILING DATE: n
 ATTORNEY/AGENT INFORMATION:
 NAME: Western, M. Wayne
 REGISTRATION NUMBER: 22,788
 REFERENCE/DOCKET NUMBER: 9325
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (801) 566-6633
 TELEFAX: (801) 566-0750
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: amino acid sequence from King Kong KKO
 NAME/KEY: conotoxin
 REFERENCE/DOCKET NUMBER: sequencer
 US-07-689-693B-17

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db ::::: 7
 DQNCDCG 7

RESULT 12
 US-07-712-828B-7
 Sequence 7, Application US/07712828B
 Patent No. 523039
 GENERAL INFORMATION:
 APPLICANT: Heath et al.
 TITLE OF INVENTION: Assay Method for Hydrolytic Enzymes
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eli Lilly and Company
 STREET: Lilly Corporate Center
 CITY: Indianapolis
 STATE: IN.

QY 1 XXXXXX 7
 US-07-663-413-25
 Sequence 25, Application US/07663413
 Patient No. 5240703
 GENERAL INFORMATION:
 APPLICANT: Cochran, Mark D.
 TITLE OF INVENTION: ATTENANTED, GENETICALLY-ENGINEERED
 PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White, Esq.
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/663,413
 FILING DATE: 19910301
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White Esq., John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE DOCKET NUMBER: 38720
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: (212) 664-0525
 TELEX: 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-663-413-25

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
 Db 1 FFOLMGK 7

RESULT 13
 US-07-663-413-20
 Sequence 20, Application US/07663413
 Patient No. 5240703
 GENERAL INFORMATION:
 APPLICANT: Cochran, Mark D.
 TITLE OF INVENTION: ATTENANTED, GENETICALLY-ENGINEERED
 PSEUDORABIES VIRUS S-PRV-155 AND USESTHEREOF
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White, Esq.
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/663,413
 FILING DATE: 19910301
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White Esq., John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE DOCKET NUMBER: 38720
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: (212) 664-0525
 TELEX: 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-663-413-25

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
 Db 1 MRWATWI 7

RESULT 15
 US-07-596-867C-8
 Sequence 8, Application US/07596867C
 Patient No. 5244796
 GENERAL INFORMATION:
 APPLICANT: Levy, H. Richard
 APPLICANT: Lee, W. Theodore
 TITLE OF INVENTION: CLONED LEUCONOSTOC MESENTEROIDES GLUCOSE-6-
 PHOSPHATE DEHYDROGENASE GENES AND METHOD OF MAKING
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wall and Roehrig
 STREET: 217 Montgomery Street
 CITY: Syracuse
 STATE: New York
 COUNTRY: United States of America
 ZIP: 13202
 COMPUTER READABLE FORM:
 Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 7; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

; MEDIUM TYPE: 5.25 inch Diskette, 360Kb storage
 ; COMPUTER: IBM Compatible PC
 ; OPERATING SYSTEM: MSDOS
 ; SOFTWARE: Word Perfect, Ver. 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/596,867C
 ; FILING DATE: 19901012
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA: No. 5244796
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bickel, Arthur S.
 ; REGISTRATION NUMBER: 34123
 ; REFERENCE/DOCKET NUMBER: 270 P 030
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (315) 422 7383
 ; TELEFAX: (315) 422 9331
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: No. 5244796 applicable
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: amino acid
 ; HYPOTHETICAL: no
 ; ANTI-SENSE: No. 5244796 applicable
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE: Leuconostoc mesenteroides glucose 6-phosphate
 ; ORIGINAL SOURCE: dehydrogenase
 ; IMMEDIATE SOURCE: No. 5244796 applicable
 ; POSITION IN GENOME: No. 5244796 applicable
 ; PUBLICATION INFORMATION: No. 5244796
 ; US-07-596-867C-8

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 XXXXXX 7
 :::::
 Db 1 ENDPEN 7

Search completed: October 28, 2003, 09:02:30
 Job time: 29 secs

GenCore version 5.1.6
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OW protein - protein search, using SW model

Run on: October 28, 2003, 08:57:32 ; Search time 39 Seconds
(without alignments)
17.261 Million cell updates/sec

Title: US-09-847-940B-6
Perfect score: 7

Sequence: 1 XXXXXXXX 7

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 961686682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	1 KEYDGD	Galactose oxidase
2	7	100.0	7	1 NYPG7	hypothalamic hepta dermorphin . Rohde fatty-acid synthas
3	7	100.0	7	1 A61324	glutathione trans
4	7	100.0	7	2 A60139	peptidyl-dipeptida
5	7	100.0	7	2 S71867	Met-enkephalin-Arg
6	7	100.0	7	2 S71867	dermorphin (Lys-7),
7	7	100.0	7	2 JN0859	Arg heavy chain V r
8	7	100.0	7	2 A60224	ribosomal protein
9	7	100.0	7	2 S36662	opacity protein P.
10	7	100.0	7	2 S21230	venom heptapeptide
11	7	100.0	7	2 PH1408	hypothetical prote
12	7	100.0	7	2 S19630	catch-relaxing pep
13	7	100.0	7	2 S16364	tryptophyllin, has
14	7	100.0	7	2 S16365	membrane protein -
15	7	100.0	7	2 A58512	RNA-directed DNA P
16	7	100.0	7	2 S088606	elastase - Pseudom
17	7	100.0	7	2 ECMUCR	tracylglycerol li
18	7	100.0	7	2 A61081	choline oxidase (E
19	7	100.0	7	2 PQ0663	hypothetical prote
20	7	100.0	7	2 S35890	microcin C7 - Esch
21	7	100.0	7	2 S20446	phosphotransferase
22	7	100.0	7	2 S57224	peptide - Esc
23	7	100.0	7	2 A15398	platelet aggregati
24	7	100.0	7	2 S09652	
25	7	100.0	7	2 S55548	
26	7	100.0	7	2 S45311	
27	7	100.0	7	2 S39127	
28	7	100.0	7	2 S25266	
29	7	100.0	7	2 A44428	

RESULT 1
KEYDGD

galactose oxidase inhibitor - fungus (Cladobotryum dendroides)

C;Species: Cladobotryum dendroides

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993

C;Accession: A01341

R;Avigad, G.; Markus, Z.

Fed. Proc. 31, 447, 1972

A;Reference number: A01341

A;Molecule type: Protein

A;Residues: 1-7 <AVI>

C;Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose ox

apoenzyme, may inactivate the enzyme by binding to its prosthetic copper group.

C;Superfamily: Galactose oxidase inhibitor

C;Keywords: copper

Query Match 100.0%; Score 7; DB 1; Length 7;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
NYPG7

hypothalamic heptapeptide - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 23-Aug-1996

C;Accession: A01417

R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong

Horm. Metab. Res. 13, 228-232, 1981

A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-rele

A;Reference number: A01417; PMID:8113980; PMID:6243778

A;Accession: A01417

A;Molecule type: Protein

A;Residues: 1-7 <CHA>

C;Superfamily: hypothalamic heptapeptide

C;Keywords: hypothalamus

Query Match 100.0%; Score 7; DB 1; Length 7;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
1 FLYSYK 7

A61324
Dermorphin - Rohde's leaf frog (Rohde's leaf frog)
C:Species: *Phyllomedusa rohdei* (Rohde's leaf frog)
C:Date: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: A61324
R:Montecuccchi, P.C.; De Castiglione, R.; Brspanier, V.
Int. J. Pept. Protein Res. 17, 316-321, 1981
A:Title: Identification of dermorphin and hyp(6)-dermorphin in skin extracts of the Brazil
A:Reference number: A61324; PMID:82029915; PMID:7287302
A:Accession: A61324
A:Molecule type: protein
A:Residues: 1-7 <MON>
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
C:Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin
F:6/Modified site: 4-hydroxyproline (Ala) #status experimental
F:7/Modified site: amidated carboxyl end (Ser) #status experimental
F:7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
Db 1 YAFGYP 7

RESULT 4
A61329
Fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C:Accession: A60139
R:Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
J.Biochem. Biophys. Acta 828, 380-382, 1985
A:Title: Amino acid sequence around the reactive serine residue of the thioesterase domain
A:Reference number: A60139; PMID:85175165; PMID:3921056
A:Accession: A60139
A:Molecule type: protein
A:Residues: 1-7 <HAR>
C:Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homolog
C:Keywords: hydrolyase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] S-acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enzyme
F:5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
Db 1 VAGYSYG 7

RESULT 5
S71867
Glutathione transferase (EC 2.5.1.18) class alpha 5 - pig (fragment)
N:Alternative names: glutathione S-transferase class alpha 5
C:Species: *Sus scrofa domestica* (domestic pig)
C:Accession: S71867
R:Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
Biochem. J. 317, 879-884, 1996
A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray
A:Reference number: S71867; PMID:96332484; PMID:870377
A:Accession: S71867
A:Molecule type: protein
A:Residues: 1-7 <MAT>
C:Comment: At least five species-independent classes of cytosolic glutathione transferases
C:Keywords: amidated carboxyl-terminal form are known.
C:Complex: dimer
C:Function: protein
A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7

A:Pathway: detoxification; xenobiotics metabolism
A:Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
es of damage
C:Superfamily: glutathione transferase
C:Keywords: dimer; transferase

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
Db 1 AILNYIA 7

RESULT 6
S71870
Glutathione transferase (EC 2.5.1.18) class mu 9 - pig (fragment)
N:Alternative names: glutathione S-transferase class mu 9
C:Species: *Sus scrofa domestica* (domestic pig)
C:Accession: S71870
R:Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
Biochem. J. 317, 879-884, 1996
A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray
A:Reference number: S71864; PMID:96332484; PMID:8760377
A:Accession: S71870
A:Molecule type: protein
A:Residues: 1-7 <ROU>
C:Comment: At least five species-independent classes of cytosolic glutathione transferases
C:Keywords: mitochondrial form are known.
C:Function: protein
A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
A:Pathway: detoxification; xenobiotics metabolism
A:Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
es of damage
C:Superfamily: dimer
C:Keywords: acetylated amino end; dimer; dimer; transferase
C:Modified site: acetylated amino end (Ser) #status experimental

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
Db 1 SMILGYA 7

RESULT 7
JN0859
peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito
C:Species: *Sarda orientalis* (striped bonito)
C:Accession: JN0859
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory F
A:Reference number: JN0859; PMID:94080036; PMID:7764272
A:Accession: JN0859
A:Molecule type: protein
A:Residues: 1-7 <MAT>
C:Experimental source: intestine
C:Comment: The carboxyl-terminal is essential for the protein's expression of angiotensin
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7

RESULT 8
 Db 1 SVAKLEK 7
 Qy 1 :::::::
 Db 1 YAFHYN 7

RESULT 9
 A6024 Met-enkephalin-Arg-Phe - rabbit (domestic rabbit)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
 C;Accession: A60244
 R;Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Makk, G.; Weber, E.
 J.; Neurochem. 56, 1914-1920, 1991
 A;Title: Isolation and characterization of opioid peptides from rabbit cerebellum.
 A;Reference number: A60244; MUID:91225680; PMID:2027006
 A;Accession: A60224
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-7 <MIG>
 C;Superfamily: proenkephalin
 C;Keywords: neuropeptide; opioid peptide

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 YGGFMRR 7

RESULT 10
 S21230 dermorphin (Lys-7) [validated] - two-colored leaf frog
 C;Species: Phyllomedusa bicolor (two-colored leaf frog)
 C;Accession: S36662
 R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspaner, G.; Kreil, G.
 FEBS Lett. 302, 151-154, 1992
 A;Title: Identification and characterization of two dermorphins from skin extracts of the
 A;Reference number: S21152; MUID:1633846
 A;Accession: S36662
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-7 <MIG>
 C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 YAFGYPK 7

RESULT 11
 PH1408 Ig heavy chain V region - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C;Accession: PH1408; PH1405
 R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.;
 J; EXP. Med. 176, 1209-1214, 1992
 A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in a virus.
 A;Reference number: PH1403; MUID:93018837; PMID:1402663
 A;Accession: PH1408
 A;Molecule type: DNA
 A;Residues: 1-7 <SH1>
 A;Experimental source: clone micro m+ 46-12-2
 A;Accession: PH1405
 A;Molecule type: DNA
 A;Residues: 1-7 <SH1>
 A;Experimental source: clone micro m+ 46-6
 C;Keywords: immunoglobulin V region; immunoglobulin homology

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 FCARRPP 7

RESULT 12
 S19630 ribosomal protein L30 - Streptomyces griseus (fragment)
 C;Species: Streptomyces griseus
 C;Accession: S19630
 R;Ochi, K.
 Int. J. Syst. Bacteriol. 42, 144-150, 1992
 A;Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete
 A;Reference number: S19630; MUID:92144363; PMID:1736962
 A;Accession: S19630
 A;Molecule type: protein
 A;Residues: 1-7 <OCH>
 A;Experimental source: strain IFO 13189
 C;Superfamily: Escherichia coli ribosomal protein L30
 C;Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 ARKIKRQ 7

RESULT 13
 S16364 opacity protein P.IIe - Neisseria gonorrhoeae (strain FA1090) (fragment)
 N;Alternate name: outer membrane protein P.IIe
 C;Species: Neisseria gonorrhoeae
 A;Variety: strain FA1090
 C;Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C;Accession: S16364
 R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;

Infect. Immun. 55, 2026-2031, 1987
 A;Title: Antigenic and structural differences among six proteins II expressed by a single
 A;Reference number: S16360; MUID:87306843; PMID:3114142
 A;Molecule type: protein
 A;Residues: 1-7 <BAR>
 A;Experimental source: strain FA1090
 A;Note: expression of opacity proteins is regulated by the number of translated repeat e
 of repeats place the start codon in frame with the rest of the protein
 C;Superfamily: opacity protein
 C;Keywords: cell surface component; transmembrane protein
 F;1-7/Product: opacity protein P.II (fragment) #status experimental <MAT>

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXX 7
 Db 1 AGEDNGR 7

RESULT 14
 S16365
 Opacity Protein P.II - *Neisseria gonorrhoeae* (strain FA1090) (fragment)
 N;Alternate names: outer membrane protein P.II
 C;Species: *Neisseria gonorrhoeae*
 C;Variety: strain FA1090
 C;Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
 C;Accession: S16365
 R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
 Infect. Immun. 55, 2026-2031, 1987
 A;Title: Antigenic and structural differences among six proteins II expressed by a singl
 A;Reference number: S16360; MUID:87306843; PMID:3114142
 A;Accession: S16365
 A;Molecule type: protein
 A;Residues: 1-7 <BAR>
 A;Experimental source: strain FA1090
 A;Note: expression of opacity proteins is regulated by the number of translated repeat e
 of repeats place the start codon in frame with the rest of the protein
 C;Superfamily: opacity protein
 C;Keywords: cell surface component; transmembrane protein
 F;1-7/Product: opacity protein P.II (fragment) #status experimental <MAT>

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXX 7
 Db 1 AGEDNGR 7

RESULT 15
 A58512
 venom heptapeptide - cone shell (*Conus imperialis*)
 C;Species: *Conus imperialis* (imperial cone)
 C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 07-May-1999
 C;Accession: A58512
 R;Craig, A.G.; Jimenez, E.C.; Dykert, J.; Nielsen, D.B.; Gulyas, J.; Abogadie, F.C.; Por
 J. Biol. Chem. 272, 4659-4658, 1997
 A;Title: A novel post-translation modification involving bromination of tryptophan. Id
 A;Reference number: A58512; MUID:97184108; PMID:9030520
 A;Molecule type: protein
 A;Residues: 1-7 <CRA>
 C;Superfamily: unassigned conotoxins
 C;Keywords: amidated carboxyl end; bromine; pyrogulamic acid; venom
 F;1;Modified site: 6-bromotryptophan (Trp) #status experimental
 F;7;Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 100.0%; Score 7; DB 2; Length 7;

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OM protein - protein search, using sw model

Run on: October 28, 2003, 08:57:28 ; Search time 93 Seconds
(without alignments)
19.423 Million cells/updates/sec

Title: US-09-847-940B-6

Perfect score: 7 Sequence: 1 XXXXXX 7

Scoring table: BLOSSM62DX Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 255052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriopl:*

17: sp_archaea:*

ALIGNMENTS

RESULT 1

QBKMS3 ID QBKMS3
QBKMS3 ; AC
01-OCT-2002 (TRMBLrel1. 22, Created)
01-OCT-2002 (TRMBLrel1. 22, Last sequence update)
01-OCT-2002 (TRMBLrel1. 22, Last annotation update)
PUTATIVE MERR2 PROTEIN.

GN MERR2
OS Klebsiella sp. LS13-39
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
RN [1]
RN NCBI_TaxID:143776;
RN

SEQUENCE FROM N A.

RC STRAIN=L-LS13-39;
RX MEDLINE=2164134; PubMed=11763242;

RA Mindlin S.Z., Kholidin G.Y., Gorlenko Z.M., Minakhina S.V.,
RA Minakhin L.S., Kalyaseva E.S., Kopteva A.V., Petrova M.A.,
RA Yurieva O.V., Nikiforov V.G.;
RT Mercury resistance transposons of Gram-negative environmental
bacteria and their classification.";
RL Res. Microbiol. 152:811-822 (2001).
DR EMBL AJ302776; CAC8:975.1; -;
SQ SEQUENCE 7 AA; 608 MN: 6DC1B5BDD87DD6F0 CRC64;

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query ID	Description
1	7	100.0	7 2 QBKMS3	QBKMS3 klebsiella
2	7	100.0	7 2 Q47505	Q47505 escherichia
3	7	100.0	7 2 P70804	P70804 zotobacter
4	7	100.0	7 2 050556	050556 actinobacil
5	7	100.0	7 2 Q47477	Q47477 escherichia
6	7	100.0	7 2 Q47029	Q47029 enterobacil
7	7	100.0	7 2 P72081	P72081 nocardia
8	7	100.0	7 2 Q54248	Q54248 streptomyce
9	7	100.0	7 2 QBKMS9	QBKMS9 enterobacil
10	7	100.0	7 2 034028	034028 sphingomonas
11	7	100.0	7 2 007354	007354 synochococcus
12	7	100.0	7 2 Q8GL12	Q8GL12 borrelia
13	7	100.0	7 2 Q8GL04	Q8GL04 borrelia
14	7	100.0	7 2 Q8GL00	Q8GL00 borrelia
15	7	100.0	7 4 Q15903	Q15903 homo sapien
16	7	100.0	7 4 Q8NHH7	Q8NHH7 homo sapien

RRESULT 2
Q47505 ID Q47505 PRELIMINARY; PRT; 7 AA.
QBKMS3 ID Q8k3n6 PRELIMINARY; PRT; 7 AA.
QBKMS3 ID Q8k3n6 PRELIMINARY; PRT; 7 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MCCA protein.
 GN MCCA.
 OS Escherichia coli.
 OG Plasmid pMCC7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9633558416; PubMed=8751884;
 RA Kolaoubetza D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C., Kraig B.; "cis Elements and trans factors are both important in strain-specific regulation of the leukotoxin gene in *Actinobacillus actinomycetemcomitans*," *Infect. Immun.* 64:3451-3460 (1996).
 RA EMBL; U51862; AAB88721.1; -.
 DR NON_TER 1 1
 FT SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
 SQ 7 AA; 763 MW; 644DD44861B406F0 CRC64;
 Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 MRTGNAN 7

RESULT 3
 P70804 PRELIMINARY; PRT; 7 AA.
 ID P70804
 AC P70804; 01-NOV-1997 (TREMBLrel. 02, Created)
 DT 01-PBB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE AlgT protein (Fragment).
 GN Azotobacter vinelandii.
 OS Azotobacter; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Azotobacter.
 OX NCBI_TaxID=354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E.
 RX MEDLINE=96427318; PubMed=8830682;
 RA Rehm H.A., Ertzsvig H., Valia S.; "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is part of an alg 9 gene cluster physically organized in a manner similar to that in *Pseudomonas aeruginosa*," *J. Bacteriol.* 178:5884-5889 (1996).
 RT Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X87973; CAA61230.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;
 Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 CTVSSST 7

RESULT 4
 OS0556 PRELIMINARY; PRT; 7 AA.
 ID OS0556
 AC OS0556; 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE GlyA (Fragment).

RESULT 5
 Q7477 PRELIMINARY; PRT; 7 AA.
 ID Q7477
 AC Q7477; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE Tp; protein (Fragment).
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Hellinga H.W., Evans P.R.; "Nucleotide sequence and high-level expression of the major *Escherichia coli* phosphofructokinase," *Biochem.* 149:363-373 (1985).
 RA Evans P.; Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
 RT EMBL; X02519; CAA26359.1; -.
 DR EMBL; X02519
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1D80 CRC64;
 Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 AEAAKQR 7

RESULT 6
 Q47029 PRELIMINARY; PRT; 7 AA.
 ID Q47029
 AC Q47029; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 01, Last annotation update)
 DE GlyA (Fragment).

DE	Aad A1 protein (Fragment).	OX	NCBI_TaxID=1911;
CN	AAD A1.	RN	(1)
CS	Enterobacter cloacae.	RP	SEQUENCE FROM N.A.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RC	STRAIN=N2-311;
OC	Enterobacteriaceae; Enterobacter.	RX	Medline=2001121; PubMed=1054230;
OC	NCBI_TaxID=550;	RA	Poehling S., Piepersberg W., Wehmeier U.F.;
RN	[1]	RA	"Analysis and regulation of the sec Y gene from Streptomyces griseus N2-3-1 and interaction of the SecY protein with the SecA protein."
RP	SEQUENCE FROM N.A.	RT	RL Biochim. Biophys. Acta 1447:298-302(1999).
RX	Medline=94079349; PubMed=8257126;	DR	EMBL: X95155; CAA65160.1; -.
RA	Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;	FT	NON-TER 1 1
RT	"Analysis of the aac(3')-V4 gene encoding a novel 3'-N-	SQ	SEQUENCE 7 AA: 760 MW: 722C72B01B2D1B2A0 CRC64;
RT	acetyltransferase."	Query Match	100.0%; Score 7; DB 2; Length 7;
RL	Antimicrob. Agents Chemother. 37:2074-2079(1993).	Best Local Similarity	0.0%; Pred. No. 0;
DR	EMBL: M88012; AAA16193.1; -.	Matches	0; Conserv. 7; Mismatches 0; Indels 0; Gaps 0;
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Db	1 ITKVVGK 7	AC	Q8KMS9;
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Db	1 VTVTELV 7	DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Qy	1 XXXXXX 7	DE	01-OCT-2002 (TrEMBLrel. 22, Last annotation update).
Db	1 VTVTELV 7	OS	Enterobacter sp. CH2-4
Qy	1 XXXXXX 7	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Db	1 ITKVVGK 7	OC	Enterobacteriaceae; Enterobacter.
Qy	1 XXXXXX 7	RN	[1]
Db	1 VTVTELV 7	RP	SEQUENCE FROM N.A.
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Db	1 ITKVVGK 7	RX	Medline=11604134; PubMed=11763242;
Qy	1 XXXXXX 7	RA	Mindlin S.Z., Khodataeva G.Y., Gorlenko Z.M., Minakhina S.V.,
Db	1 ITKVVGK 7	RA	Minakhina L.S., Kalyasva E.S., Kopteva A.V., Petrova M.A.,
Qy	1 XXXXXX 7	RA	Yurieva O.V., Nikiforov V.G.;
Db	1 ITKVVGK 7	RT	Mercury resistance transposons of Gram-negative environmental
Qy	1 XXXXXX 7	RT	bacteria and their classification."
Db	1 ITKVVGK 7	RL	Res. Microbiol. 152:811-822(2001).
Qy	1 XXXXXX 7	DR	EMBL: AJ302778; CAC81058.1; -.
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Db	1 ITKVVGK 7	Query Match	100.0%; Score 7; DB 2; Length 7;
Qy	1 XXXXXX 7	Best Local Similarity	0.0%; Pred. No. 0;
Db	1 ITKVVGK 7	Matches	0; Conserv. 7; Mismatches 0; Indels 0; Gaps 0;
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Qy	1 XXXXXX 7	DT	01-JAN-1998 (TrEMBLrel. 05, Created)
Db	1 ITKVVGK 7	DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
Qy	1 XXXXXX 7	DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Db	1 ITKVVGK 7	DB	Catechol-2,3-dioxygenase (Fragment).
Qy	1 XXXXXX 7	GN	Shingomonas chungbukensis.
Db	1 ITKVVGK 7	OS	Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Qy	1 XXXXXX 7	OC	Shingomonadaceae; Sphingomonas.
Db	1 ITKVVGK 7	OC	NCBI_TaxID=6193;
Qy	1 XXXXXX 7	RN	[1]
Db	1 ITKVVGK 7	RP	SEQUENCE FROM N.A.

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RC STRAIN=DJ77;
RA Kim Y.-C.
RA Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RL EMBL; U88208; AB66311.1; -
DR Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae
KW Dioxygenase.
DN NON-TER.
FT 1 1
SQ 7 AA; 868 MN; 71A452D1A699D160 CRC64;
  Query Match 100.0%; Score 7; DB 2; Length 7;
  Best Local Similarity 0.0%; Pred. No. 0;
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  Db 1 RFMTVNT 7

RESULT 11
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  ID O07354;
  AC AC007354;
  DT 01-JUL-1997 (TREMBLrel. 04, Created)
  DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
  DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
  DE NIEK (Fragment).
  RN 1
  OS Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanophyceae)
  OC Bacteria; Cyanobacteria; Chroococcales; Cyanophyceae.
  NCBI_TaxID=41431;
  RN [1]
  REP SEQUENCE FROM N.A.
  STRAIN=RF-1.
  RX MEDLINE=9231861; PubMed=10217509;
  RA Huang T.C.; Lin R.F.; Chu M.K.; Chen H.M.;
  PT "Organization and expression of nitrogen-fixation genes
  RT nitrogen-fixing unicellular cyanobacterium Synechococcus
  RT RF-1."
  DR AF003700; AAC35193.1; -
  FT 1
  SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;

  Query Match 100.0%; Score 7; DB 2; Length 7;
  Best Local Similarity 0.0%; Pred. No. 0;
  Matches 0; Conservative 7; Mismatches 0; Indels 0
  Qy 1 XXXXXXXX 7
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RESULT 12
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  ID Q8GL12;
  AC Q8GL12;
  DT 01-MAR-2003 (TREMBLrel. 22, Created)
  DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
  DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
  DE PF-50 protein (Fragment).
  RN 1
  OS Borrelia burgdorferi (Lyme disease spirochete).
  OG Plasmid group C32-9.
  OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae
  NCBI_TaxID=139;
  RN [1]
  REP SEQUENCE FROM N.A.
  STRAIN=N40;
  RA Miller J.C.; Stevens B.; Miller J.C.; Burgdorferi
  PT Comparative analyses of Borrelia burgdorferi erp genes
  RT prokaryotes: conservation amidst diversity.
  RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
  DR EMBL; AA142100; AAN17911; -
  RL Plasmid.

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RESULT 13									
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AC	Q8GL04;								
DT	01-MAR-2003	(TREMBLrel.	23;			Created)			
DT	01-MAR-2003	(TREMBLrel.	23;			Last sequence update)			
DT	01-MAR-2003	(TREMBLrel.	23;			Last annotation update)			
DE	PF-550	protein (Fragment).							
GN	PF-550.								
OS	Borrelia burgdorferi	(Lyme disease spirochete).							
OC	Plasmid group CP32-5.								
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.								
OX	NCBI_TaxID=139;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=93-0107;								
RA	Stevenson B., Miller J.C.,					Borrelia burgdorferi	erp	genes and their cp32	
RT	"Comparative analyses of Borrelia burgdorferi					erp genes and their cp32			
RT	prophages: conservation amidst diversity";								
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.								
RL	EMBL; AY142103; AAN17848.1; -.								
DR									
KW	Plasmid.								
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SQ	SEQUENCE	7	AA;	914	MW;	6337244330504310	CRC64;		
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Db	1	WIKINLK	7						
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ID	O8GL00								
AC	Q8GL00;								
DT	01-MAR-2003	(TREMBLrel.	23;			Created)			
DT	01-MAR-2003	(TREMBLrel.	23;			Last sequence update)			
DT	01-MAR-2003	(TREMBLrel.	23;			Last annotation update)			
DE	PF-50	protein (Fragment).							
GN	PF-50.								
OS	Borrelia burgdorferi	(Lyme disease spirochete).							
OC	Plasmid group CP32-13.								
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.								
OX	NCBI_TaxID=139;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=CR15;								
RA	Stevenson B., Miller J.C.,					Borrelia burgdorferi	erp	genes and their cp32	
RT	"Comparative analyses of Borrelia burgdorferi					erp genes and their cp32			
RT	prophages: conservation amidst diversity";								
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.								
RL	EMBL; AY142106; AAN17857.1; -.								
KW	Plasmid.								
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Best Local Similarity	0.0%					Pred. No. 0;			

Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 RWIKLK 7

RESULT 15
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 ID Q15903; AC DT 01-NOV-1996 (TRIMBLrel. 01, Created); DT 01-NOV-1996 (TRIMBLrel. 01, Last sequence update); DT 01-DEC-2001 (TRIMBLrel. 19, Last annotation update); DE (Clone XP787); OS Homo sapiens (Human); OC Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TaxID=9606; RN (1); RP SEQUENCE FROM N.A.

RC TISSUE=Placenta; RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baidani A., Lindsay S.A., Zhao Z.-Y., Caskey C.T.H.; RT "Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.,"; RT RL Mol. Genet. 0:0-0(1995).; DR EMBL: L32082; AAAT73893.1; -; FT NON-TER 1 1; FT NON-TER 7 7; SQ SEQUENCE 7 AA; 849 MW; 6B040339CDD33DB0 CRC64;

Query Match 100.0%; Score 7; DB 4; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
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 Db 1 AKAFKRE 7

Search completed: October 28, 2003, 08:59:44
 Job time : 98 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 09:01:17 ; Search time 366 Seconds
(without alignments)
3.203 Million cell updates/sec

Title: US-09-847-940B-6

Perfect score: 7 Sequence: 1 XXXXXX 7

Scoring table: BLOSUM62DX Gapext 0.5

Searched: 629382 seeds, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	7	100.0	7	7 US-09-765-837-7	Sequence 7, App1
2	7	100.0	7	7 US-09-344-824-53	Sequence 53, App1
3	7	100.0	7	7 US-09-996-140-4	Sequence 4, App1
4	7	100.0	7	7 US-09-996-140-17	Sequence 17, App1
5	7	100.0	7	8 US-09-859-699-14	Sequence 14, App1
6	7	100.0	7	8 US-09-859-699-22	Sequence 2, App1
7	7	100.0	7	8 US-09-812-393A-51	Sequence 51, App1
8	7	100.0	7	8 US-09-967-573A-4	Sequence 4, App1
9	7	100.0	7	8 US-09-967-573A-5	Sequence 5, App1
10	7	100.0	7	8 US-09-967-573A-12	Sequence 12, App1
11	7	100.0	7	8 US-09-967-573A-13	Sequence 13, App1
12	7	100.0	7	8 US-09-967-573A-14	Sequence 14, App1
13	7	100.0	7	8 US-09-967-573A-15	Sequence 15, App1
14	7	100.0	7	8 US-09-967-573A-16	Sequence 16, App1
15	7	100.0	7	8 US-09-967-573A-17	Sequence 17, App1

RESULT 1 US-09-765-837-7
; Sequence 7, Application US/08765837
; Publication No. US2003147900A1
; GENERAL INFORMATION:
; APPLICANT: LAUB, RUTH
; APPLICANT: DI GAMBATISTA, MARIO
; TITLE OF INVENTION: ANTIGENIC POLYPEPTIDE SEQUENCE
; TITLE OF INVENTION: OF FACTOR VIII, AND FRAGMENTS AND/OR
; NUMBER OF SEQUENCES: 20
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,837
; FILING DATE: 14-JUL-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/B695/00068
; FILING DATE: 14-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: VANMA48.001APC
; TELECOMMUNICATION INFORMATION:
; TELEFAX: 714-760-3502
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:

ALIGNMENTS

SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. US20030147900A1
 FRAGMENT TYPE: internal
 US-08-765-837-7

Query Match 100.0%; Score 7; DB 7; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Gaps 0;
 SEQ ID NO: 53

Qy 1 XXXXXX 7
 Db 1 ETKSWYF 7

RESULT 2
 US-08-344-824-53
 Sequence 53, Application US/08344824
 Publication No US20030152580A1
 GENERAL INFORMATION:
 APPLICANT: SETTE, Alessandro
 TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
 NUMBER OF SEQUENCES: 399
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Steuart Street Tower, 20th
 STREET: Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/344,824
 FILING DATE: 23-NOV-1994
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/278,634
 FILING DATE: 21-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 14137-80-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-344-824-53

Query Match 100.0%; Score 7; DB 7; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Gaps 0;
 SEQ ID NO: 53

Qy 1 XXXXXX 7
 Db 1 ETKSWYF 7

RESULT 4
 US-08-996-140-4
 Sequence 4, Application US/08996140
 Publication No. US20030190318A1
 GENERAL INFORMATION:
 APPLICANT: TORIGOE, Kakaji
 APPLICANT: USHIO, Shimpel
 APPLICANT: KUNIKATA, Masshi
 APPLICANT: KURIMOTO, Masshi
 TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/996,140
 FILING DATE: 22-DEC-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 356,426/1996
 FILING DATE: 26-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 52,526/1997
 FILING DATE: 21-FEB-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 163,490/1997
 FILING DATE: 6-JUN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 215,490/1997
 FILING DATE: 28-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: Internal fragment
 US-08-996-140-4

Query Match 100.0%; Score 7; DB 7; Length 7;
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Qy 1 XXXXXX 7
 Db 1 IMPEFGK 7

RESULT 4
 US-08-996-140-17
 Sequence 17, Application US/08996140
 Publication No. US20030190318A1
 GENERAL INFORMATION:
 APPLICANT: TORIGOE, Kakaji
 APPLICANT: USHIO, Shimpel
 APPLICANT: KUNIKATA, Masshi
 APPLICANT: KURIMOTO, Masshi
 TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
 NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOCS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/996,140
 FILING DATE: 22-DEC-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 356,426/1996
 FILING DATE: 26-DEC-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 52,526/1997
 FILING DATE: 21-FEB-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 163,490/1997
 FILING DATE: 6-JUN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 215,490/1997
 FILING DATE: 28-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: TORIGOE=2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 SEQUENCE FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: Internal fragment
 US-08-996-140-17

Query Match 100.0%; Score 7; DB 7; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 XXXXXXX 7
 :::::::
 Db 1 NAKTLAD 7

RESULT 5
 US-08-859-699-14
 Sequence 14, Application US/08859699A
 Publication No. US20010007017A1
 GENERAL INFORMATION:
 APPLICANT: VELJKOVIC, Veljko
 ; TITLE OF INVENTION: PEPTIDES WHICH REACT WITH ANTI BODY REPRESENTING THE
 ; TITLE OF INVENTION: PEPTIDES WHICH REACT WITH ANTI BODY REPRESENTING THE
 ; FILE REFERENCE: VELJKOVIC et al. 08/859,699
 ; CURRENT APPLICATION NUMBER: US/08/859,699A
 ; CURRENT FILING DATE: 1997-05-21
 ; EARLIER APPLICATION NUMBER: GB 9610673.7
 ; EARLIER FILING DATE: 1996-05-22
 ; EARLIER APPLICATION NUMBER: GB 9623340.8
 ; EARLIER FILING DATE: 1996-11-08
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 22
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Derivative of
 ; OTHER INFORMATION: NTM peptide.
 US-08-859-699-22

Query Match 100.0%; Score 7; DB 8; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 XXXXXXX 7
 :::::::
 Db 1 IVQLES 7

RESULT 7
 US-08-812-393A-51
 Sequence 51, Application US/08812393A
 Publication No. US2001007152A1
 GENERAL INFORMATION:
 APPLICANT: SHERMAN, Linda A.
 ; APPLICANT: LUSCIGARTEN, Joseph
 ; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING
 ; TITLE OF INVENTION: T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1888
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS

RESULT 10
 US-08-967-573A-12
 Sequence 12, Application US/08967573A
 Publication No. US20010048926A1
 GENERAL INFORMATION:
 APPLICANT: Smith, Daniel J.
 APPLICANT: Taubman, Martin A.
 TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
 TITLE OF INVENTION: FOR DENTAL CARRIES
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/967,573A
 FILING DATE: 10-NOV-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/057,162
 FILING DATE: 30-APR-1993
 APPLICATION NUMBER: 07/877,295
 FILING DATE: 07/877,295
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/057,162
 FILING DATE: 30-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: FDC92-01A2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-9240
 TELEFAX: 781-861-9540
 TELEX:
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-967-573A-13

Query Match 100.0%; Score 7; DB 8; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 XXXXXX 7
 Db 1 GYEFLI 7

RESULT 12
 US-08-967-573A-14
 Sequence 14, Application US/08967573A
 Publication No. US20010048926A1
 GENERAL INFORMATION:
 APPLICANT: Smith, Daniel J.
 APPLICANT: Taubman, Martin A.
 TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
 TITLE OF INVENTION: FOR DENTAL CARRIES
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/967,573A
 FILING DATE: 10-NOV-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/057,162
 FILING DATE: 30-APR-1993
 APPLICATION NUMBER: 07/877,295
 FILING DATE: 07/877,295
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/057,162
 FILING DATE: 30-APR-1993
 APPLICATION NUMBER: 07/877,295
 FILING DATE: 01-MAY-1992

RESULT 11
 US-08-967-573A-13
 Sequence 13, Application US/08967573A
 Publication No. US20010048926A1
 GENERAL INFORMATION:
 APPLICANT: Smith, Daniel J.
 APPLICANT: Taubman, Martin A.
 TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
 TITLE OF INVENTION: FOR DENTAL CARRIES
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: MA

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32-227
; REFERENCE/DOCKET NUMBER: FDC92-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-573A-14
Query Match 100.0%; Score 7; DB 8; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Qy 1 XXXXXX 7
Db 1 YEFLIAN 7

; RESULT 14
; US-08-967-573A-16
; Sequence 16, Application US/08967573A
; Publication No. US20010048926A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES
; TITLE OF INVENTION: FOR DENTAL CARIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967, 573A
; APPLICATION NUMBER: US/08/967, 573A
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/057, 162
; APPLICATION NUMBER: 08/057, 162
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: 07/877, 295
; FILING DATE: 01-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REFERENCE/DOCKET NUMBER: FDC92-01A2
; REGISTRATION NUMBER: 32-227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-573A-16
Query Match 100.0%; Score 7; DB 8; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Qy 1 XXXXXX 7
Db 1 LANDVDN 7

; RESULT 15
; US-08-967-573A-17
; Sequence 17, Application US/08967573A
; Publication No. US20010048926A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; MOLECULE TYPE: peptide
US-08-967-573A-15
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

```

APPLICANT: Taubman, Martin A. SYNTHETIC PEPTIDE VACCINES
TITLE OF INVENTION: FOR DENTAL CARIES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,573A
FILING DATE: 10-NOV-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/057,162
FILING DATE: 30-APR-1993
APPLICATION NUMBER: 07/877,295
FILING DATE: 01-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: FDC92-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-967-573A-17

Query Match Score 7; DB 8; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0;
Indels 0; Gaps 0;
Qy 1 XXXXXX 7
Db 1 ::::: 1 ANDVNS 7

Search completed: October 28, 2003, 09:17:12
Job time: 366 secs

PT Immunostimulant medicaments contg. thymosin, alpha-1 peptide
PR fragment - e.g. seryl-aspartyl-alanyl-alanyl-valyl-aspartic acid
XX
XX
Claim 26; Page 53; 68pp; German.

CC The inventors claim new medicaments with immunostimulant activity.
CC They contain at least one thymosin alpha-1 fragment and/or
CC derivative. The N-terminal of the fragments carry a 1-6 C acyl or
CC (1-6 C acyl)-glycyl gp. The Glu residues may be present as amides
CC or 1-6 C alkylamides and/or the asparagine or aspartic-acid residues
CC are present as the amide, 1-6 C alky1-amide, diamide or di(1-6 C
CC alky1 amide).
CC (Updated on 16-AUG-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)

Sequence 7 AA;
Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0;
Gaps 0;
SQ
Qy 1 XXXXXXX 7
Db 1 TKDLKEK 7

RESULT 2
AAP10170
ID AAP10170 standard; peptide; 7 AA.
XX
AC AAP10170;
XX
AC
XX
DT 19-AUG-1992 (first entry)
XX
DE Sequence which corresp. to AAs 325-332 of the C4 isozyme of lactate
dehydrogenase found in mammalian sperm.
XX
KW Vaccine; contraceptive; fertility reduction.
XX
OS Mammal.
XX
PN US4230944-A.
XX
PD 22-SEP-1981.
XX
PP 31-JUL-1980; 80US-0174011.
XX
PR 31-JUL-1980; 80US-0174011.
PR 01-JAN-1981; 81WO-001211.
PR 01-JAN-1981; 81AU-0076459.
PR 21-SEP-1981; 81EP-0902712.
PR 01-JAN-1981; 81JP-050325.
PR 11-MAY-1983; 83DK-0002120.
PR 16-SEP-1981; 81CA-0386098.
XX
PA (NOUN) NORTHWESTERN UNIV.
PA (GOLD) GOLDBERG E.
XX
PI Goldberg E;
XX
DR WPI; 1981-75566D/41 (75566D).
XX
PR Antigenic linear hexapeptide - useful for conjugation to protein
PR carrier for vaccine to reduce fertility of mammals
XX
PS Claim 1; column 4; 3pp; English.

CC The peptide of the invention is an antigen for use in a vaccine for
CC reducing the fertility of mammals. It is conjugated to a carrier
CC molecule, pref. a protein which itself elicits an antigenic response
CC and can be safely administered, e.g. to tetanus toxoid for
CC intramuscular admin., pref. to human females, when antibodies are

CC Formed and appear in the oviduct fluid. Dose is 1-10 mg.
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0;
Gaps 0;
Qy 1 XXXXXXX 7
Db 1 MQKDEL 7

RESULT 3
AAP10039
ID AAP10039 standard; peptide; 7 AA.
XX
AC AAP10039;
XX
DT 25-OCT-1992 (first entry)
XX
DE Sequence of peptides with immunopotentiating function.
XX
KW Immunopotentiating agent; thymus-dependent lymphocyte; regulation;
KW differentiation.
XX
OS Synthetic.
XX
PN EP26464-A.
XX
PD 08-APR-1981.
XX
PF 11-AUG-1982; 82EP-0407222.
XX
PR 28-APR-1980; 80US-0144516.
PR 28-SEP-1979; 79US-0079630.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
PA (SPAR-) SPARAMEDICA AG.
XX
PI Meienhofer JA;
XX
DR WPI; 1981-27641D/16 (27641D).
XX
PT Peptide derivs. contg. Glutamic acid and asparagine - useful as
PT immuno-potentiating agents by effect on T-cells
XX
PS Claim 7; Page 25; 31pp; German.

CC The sequence in AAP10039 is in claim 7. Preceding claims claim
CC fragments of AAP10039 comprising residues 2-7, 3-7, 4-7, 5-7 and 6-7.
CC AAP10039 and its fragments and their pharmaceutically acceptable salts
CC influence the regulation, differentiation and function of thymus-
CC dependent lymphocytes, and so are useful as immunopotentiating
CC agents when administered parenterally at 0.1-50 mg./kg. The tri- and
CC penta-peptide fragments are esp. pref. cpds.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0;
Gaps 0;
Qy 1 XXXXXXX 7
Db 1 VVEEREN 7

RESULT 4
AAP10156
ID AAP10156 standard; peptide; 7 AA.
XX
AC AAP10156;

CC themselves lost the ability to liberate insulin from the Langerhans
 CC islets.
 XX Sequence 7 AA;
 SQ

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXX 7
 DB 1 SARLZRL 7

RESULT 9
 AAP10583
 ID AAP10583 standard; peptide; 7 AA.
 XX
 AC AAP10583;
 XX
 DT 25-MAR-2003 (updated)
 DT 22-DEC-1992 (first entry)
 DE Analgesic peptide #39.
 XX
 KW Growth Hormone release; prolactin; painkiller; anti-psychotic.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Location/Qualifiers
 FT Misc-difference 2 /note= "D-Ala"
 FT Modified-site 5 /note= "Bzl-protected if Ser at position 7
 is Bzl-protected"
 FT Modified-site 6 /label= OTHER
 FT Modified-site 7 /note= "hydroxyproline"
 FT
 FT /note= "Ser-NH2 or Ser (Bzl)-NH2 if Tyr at
 position 5 is Bzl-protected"
 XX
 BE885283-A.
 XX
 PD 18-MAR-1981.
 XX
 PR 19-SEP-1980; 80BE-0983143.
 XX
 PR 09-MAY-1980; 80GB-0015412.
 PR 20-SEP-1979; 79GB-0032590.
 PR 20-SEP-1978; 78GB-0032590.
 PR 17-SEP-1980; 80GB-0029999.
 XX
 (FARM) FARMITALIA ERBA SPA CARLO.
 PA Decastigli R, Faoro F, Perseo G, Piani S, Santagelo F;
 PI
 PR 1981-23404D/14 (23404D).
 XX
 PR Analgesic and antipsychotic polypeptide(s) - also useful in neuro
 PT endocrinology and to stimulate liberation of Growth Hormone and
 PT prolactin.
 PT Example; Page 14; 41PP; French.
 XX
 PR Peptides covered by this sequence are preferred examples of a highly
 PT generic formula for peptides with analgesic and antipsychotic
 PR properties. The peptides also have Growth Hormone releasing and
 XX prolactin releasing properties. The peptides whose Nterminus is
 PR Boc-protected are in the form of their hydrochloride salts.
 CC See AAP10545-P10584.
 CC (Updated on 22-MAR-2003 to correct PA field.)
 CC (Updated on 23-MAR-2003 to correct PI field.)
 XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXXX 7
 Db 1 YAFGFP 7

RESULT 11
 ID AAP10564 standard; peptide: 7 AA.
 AC
 XX
 DT 25-MAR-2003 {updated)
 DR 22-DEC-1992 (first entry)
 DE
 XX
 KW Growth Hormone release; prolactin; painkiller; anti-psychotic.
 XX
 OS Synthetic.
 FH
 FR Key
 FR Modified-site 1
 FR Location/Qualifiers
 /note= "opt. Boc-protected when Ser at position 7
 is Ser-NH2 or Ser-NHNH2"
 FR Misc-difference 2
 FR /note= "D-Ala"
 FR Modified-site 5
 FR /note= "opt. Bzl-protected when Ser at position 7
 is Ser-NH2 or Ser(Bzl) NH2"
 FR Modified-site 7
 FR /note= "Ser-OH, Ser-NH2, Ser-Ome, Ser-NHMe,
 Ser-NHET, Ser-NH-CH(CH3)2, Ser-NHNHZ or
 Ser-NHNH2"
 FR XX
 PN BE885283-A.
 XX
 PD 18-MAR-1981.
 XX
 PR 19-SEP-1980; 80BE-0983143.
 XX
 PR 09-MAY-1980; 80GB-0015412.
 PR 20-SEP-1979; 79GB-0012590.
 PR 20-SEP-1978; 78GB-0032590.
 PR 17-SEP-1980; 80GB-0029999.
 XX
 PA (FARM) FARMITALIA ERBA SPA CARLO.
 PA XX
 PI Decastigli R, Faoro F, Perseo G, Piani S, Santagelo F;
 PI XX
 DR 1981-23404D/14 (23404D).
 PR XX
 PR Analgesic and antipsychotic polypeptide(s) - also useful in neuro
 PR endocrinology and to stimulate liberation of growth hormone and
 PR prolactin
 XX
 PS Example: Page 12; 41pp; French.
 XX
 CC Peptides covered by this sequence are preferred examples of a highly
 CC generic formula for peptides with analgesic and antipsychotic
 CC properties. The peptides also have Growth Hormone releasing and
 CC prolactin releasing properties. The peptide whose N-terminus is not
 CC Boc-protected is in the form of its hydrochloride salt.
 CC See AAP10545-P10584.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 7 AA;
 CC
 CC Peptides covered by this sequence are preferred examples of a highly
 CC generic formula for peptides with analgesic and antipsychotic
 CC properties. The peptides also have Growth Hormone releasing and
 CC prolactin releasing properties. Peptides whose N-terminus is not
 CC Boc-protected and whose C-terminus is Ser-NH2 may be in
 CC the form of their hydrochloride or trifluoroacetic acid salts; the
 CC peptide with Ser-NHNHZ at position 7 and lacking a Boc-protecting
 CC group the N-terminus is in the form of its hydrochloride salt
 CC and the peptides with Ser-Ome, Ser-OH, Ser-NHMe or Ser-NH2 at
 CC position 7 are in the form of their hydrochloride salts.
 CC See AAP10545-P10584.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 XXXXXX 7
 Db 1 YAFGFP 7

RESULT 12
 ID AAP10565 standard; peptide: 7 AA.
 XX
 AC AAP10565;
 XX
 DT 25-MAR-2003 {updated)
 DR 22-DEC-1992 (first entry)
 XX
 DE
 XX
 KW Growth Hormone release; prolactin; painkiller; anti-psychotic.
 XX
 OS Synthetic.
 FH
 FR Key
 FR Modified-site 1
 FR /note= "opt. Boc-protected"
 FR Misc-difference 2
 FR /note= "D-Ala"
 FR Modified-site 7
 FR /note= "Ser-NH2"
 XX
 PN BE885283-A.
 XX
 PD 18-MAR-1981.
 XX
 PR 19-SEP-1980; 80BE-0983143.
 XX
 PR 09-MAY-1980; 80GB-0015412.
 PR 20-SEP-1979; 79GB-0032590.
 PR 20-SEP-1978; 78GB-0032590.
 PR 17-SEP-1980; 80GB-0029999.
 XX
 PA (FARM) FARMITALIA ERBA SPA CARLO.
 PA XX
 PI Decastigli R, Faoro F, Perseo G, Piani S, Santagelo F;
 PI XX
 DR 1981-23404D/14 (23404D).
 PR XX
 PR Analgesic and antipsychotic polypeptide(s) - also useful in neuro
 PR endocrinology and to stimulate liberation of growth hormone and
 PR prolactin
 XX
 PS Example: Page 13; 41pp; French.
 XX
 CC Peptides covered by this sequence are preferred examples of a highly
 CC generic formula for peptides with analgesic and antipsychotic
 CC properties. The peptides also have Growth Hormone releasing and
 CC prolactin releasing properties. The peptide whose N-terminus is not
 CC Boc-protected is in the form of its hydrochloride salt.
 CC See AAP10545-P10584.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 7 AA;
 CC
 CC Peptides covered by this sequence are preferred examples of a highly
 CC generic formula for peptides with analgesic and antipsychotic
 CC properties. The peptides also have Growth Hormone releasing and
 CC prolactin releasing properties. Peptides whose N-terminus is not
 CC Boc-protected and whose C-terminus is Ser-NH2 may be in
 CC the form of their hydrochloride or trifluoroacetic acid salts; the
 CC peptide with Ser-NHNHZ at position 7 and lacking a Boc-protecting
 CC group the N-terminus is in the form of its hydrochloride salt
 CC and the peptides with Ser-Ome, Ser-OH, Ser-NHMe or Ser-NH2 at
 CC position 7 are in the form of their hydrochloride salts.
 CC See AAP10545-P10584.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0;
 Indels 0; Gaps 0;

XX Key Location/Qualifiers
 FH Misc-difference 2
 FT /note= "D-Ala"
 FT Modified-site 5
 FT /note= "phe(N02) or p-fluorophe"
 FT Modified-site 7
 FT /note= "Ser-NH2"
 XX BE885283-A.
 XX PD 18-MAR-1981.
 XX PP 19-SEP-1980; 80BE-0983143.
 XX PR 09-MAY-1980; 80GB-0015412.
 XX PR 20-SEP-1979; 79GB-0032590.
 XX PR 20-SEP-1978; 78GB-002590.
 XX PR 17-SEP-1980; 80GB-0029999.
 PA (FARM) FARMITALIA ERBA SPA CARLO.
 XX PI Decastiglio R, Faoro F, Perseo G, Piani S, Santagelo F;
 XX DR 1981-23404D/14 (23404D).
 XX PT Analgesic and antipsychotic polypeptide(s) - also useful in neuro
 PT endocrinology and to stimulate liberation of growth hormone and
 PT prolactin
 XX PS Example: Page 13; 41pp; French.
 XX Peptides covered by this sequence are preferred examples of a highly
 CC generic formula for peptides with analgesic and antipsychotic
 CC properties. The peptides also have Growth Hormone releasing and
 CC prolactin releasing properties. The peptide in which Phe(5) is
 CC see AAP1055-P10584.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 7; DB 2; Length 7;
 Best Local Similarity 0.0%; Prd. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 XXXXXX 7
 :::::
 Db 1 YAFGFP 7

Search completed: October 28, 2003, 09:01:08
 Job time : 81 secs

Scoring table:	BLOSUM62DX	Gapext 0.5	34	7	100.0	7	1	UH11_RAT
Searched:	127863 seqs, 47026705 residues		35	7	100.0	7	1	UN06_PINPS
Total number of hits satisfying chosen parameters:	127863		36	7	100.0	7	1	WKA1_ACHFU
Minimum DB seq length: 0			37	7	100.0	7	1	WKA2_ACHFU
Maximum DB seq length: 2000000000			38	7	100.0	7	1	WKA3_ACHFU
Post-processing: Minimum Match 0%			39	7	100.0	8	1	ACT_TNDAL
Maximum Match 100%			40	7	100.0	8	1	ACT_CARNA
Listing First 45 summaries			41	7	100.0	8	1	AKH_GRYBI
Database :	SwissProt_41:*		42	7	100.0	8	1	AKH_EFRAU
Perfect score: 7			43	7	100.0	8	1	AKH_MELML
Sequence: 1 XXXXXX 7			44	7	100.0	8	1	AKH_TABAT
			45	7	100.0	8	1	AL12_CARMA
ALIGNMENTS								
RESULT 1								
ALL2_CARMA	ID	ALL2_CARMA	STANDARD;	PRT;	7 AA.			
AC	P81805;							
DR	30-MAY-2000 (Rel. 39, Created)							
DT	30-MAY-2000 (Rel. 39, Last sequence update)							
DT	30-MAY-2000 (Rel. 39, Last annotation update)							
DE	Carcinustatin 2.							
OS	Carcinus maenas (Common shore crab) (Green crab).							
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;							
OC	Eumalacostraca; Eucarida; Decapoda; Ploocymenata; Brachyura;							
OC	Bubrachyura; Portunoidea; Portunidae; Carcinus.							
OX	NCBI_TaxID=6759;							
RN	[1]							
RP	SEQUENCE.							
RC	SEQUENCE=Cerebral ganglion, and Thoracic ganglion;							
RX	Medline=98121133; PubMed=9461295;							
RA	Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;							
RA	"Isolation and identification of multiple neuropeptides of the							
RT	allatostatin superfamily in the shore crab <i>Carcinus maenas</i> ."							
RL	Bur. J. Biochem. 250:727-734(1997).							
CC	-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.							
CC	-!- SIMILARITY: BELONGS TO THE ALLATOININ FAMILY.							
KW	Neuropeptide; Amidation; Multigene family.							
FT	MOD RES	7	7	7	7	7	7	AMIDATION (POTENTIAL).
SQ	SEQUENCE	7 AA;	770 MW;	672879CDCB5DB70	CRC64;			
Query Match	100.0%	Score 7; DB 1; Length 7;						
Best Local Similarity	0.0%	Pred. No. 0;						
Matches	0;	Conservative 7; Mismatches 0;						
Indels	0;	Gaps 0;						
Oy	1 XXXXXX 7							
Db	1 EAYAFGL 7							
SUMMARIES								
Result No.	Score	Query Match	Length	DB	ID	Description		
1	7	100.0	7	1	ALL2_CARMA	P81805 carcinus ma		
2	7	100.0	7	1	ALL3_CARMA	P81806 carcinus ma		
3	7	100.0	7	1	ALL4_CARMA	P81807 carcinus ma		
4	7	100.0	7	1	ALL5_CARMA	P81808 carcinus ma		
5	7	100.0	7	1	ALL7_CYDPO	P82158 cydia ponon		
6	7	100.0	7	1	BRHP_CONDIM	P58803 conus imper		
7	7	100.0	7	1	CARP_MYTCD	P10420 mytilus edu		
8	7	100.0	7	1	CCPE_ENTPA	P20104 enterococcus		
9	7	100.0	7	1	CHOX_ALCSP	P16101 alcaligenes		
10	7	100.0	7	1	CIA_ENTPA	P11932 enterococcus		
11	7	100.0	7	1	E105_LIPRU	P82101 littoria rub		
12	7	100.0	7	1	FAR1_ASCDQ	P31889 ascaris suu		
13	7	100.0	7	1	FAR1_HELT1	P41871 helisoma tr		
14	7	100.0	7	1	FAR1_MACRS	P83274 macrobrachii		
15	7	100.0	7	1	FAR1_PROCL	P38498 procambiarus		
16	7	100.0	7	1	FAR2_ASCSU	P31890 ascaris suu		
17	7	100.0	7	1	FAR2_PROCL	P38498 procambiarus		
18	7	100.0	7	1	FAR3_HAEZ	P81298 haemochilus		
19	7	100.0	7	1	FAR3_PANFE	P41874 panagrellus		
20	7	100.0	7	1	FAR4_PANFE	P41875 panagrellus		
21	7	100.0	7	1	FAR5_HIRNE	P42544 hirudo medi		
22	7	100.0	7	1	FAR8_CALVO	P41866 calliphora		
23	7	100.0	7	1	GFRP_MOISE	P99025 mus musculu		
24	7	100.0	7	1	HY2_BIG	P01153 sus scrofa		
25	7	100.0	7	1	IGA0_DACDB	P06294 dactylium d		
26	7	100.0	7	1	LANC_CARU	P36960 carnobacter		
27	7	100.0	7	1	MNP1_LEPPE	P42984 leptinotarsa		
28	7	100.0	7	1	PPH2_LYCES	P83379 lycopersico		
29	7	100.0	7	1	TPFY_PACNA	P83455 pachymedusa		
30	7	100.0	7	1	TY51_LITPA	P82065 littoria rub		
31	7	100.0	7	1	UC24_MA12B	P80630 zea mays (m		
32	7	100.0	7	1	UF03_MOUSE	P38641 mus musculu		
33	7	100.0	7	1	UF04_MOUSE	P38642 mus musculu		
RESULT 2								
ALL3_CARMA	ID	ALL3_CARMA	STANDARD;	PRT;	7 AA.			
AC	P81805;							
DT	30-MAY-2000 (Rel. 39, Created)							
DT	30-MAY-2000 (Rel. 39, Last sequence update)							
DT	30-MAY-2000 (Rel. 39, Last annotation update)							
DE	Carcinustatin 3.							
OS	Carcinus maenas (Common shore crab) (Green crab).							
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;							
OC	Eumalacostraca; Eucarida; Decapoda; Ploocymenata; Brachyura;							
OC	Bubrachyura; Portunoidea; Portunidae; Carcinus.							
OX	NCBI_TaxID=6759;							
RN	[1]							
RP	SEQUENCE.							
RC	SEQUENCE=Cerebral ganglion, and Thoracic ganglion;							
RX	Medline=98121133; PubMed=9461295;							
RA	Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;							

"Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RT Eur. J. Biochem. 250:727-734 (1997).
 RL -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Multigene family.
 SQ SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;

Query Match 100.0% Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0; Indels 0; Gaps 0;
 Matches 0; Conservative 7; Mismatches 0; Delmiss 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 EPYAFGL 7

RESULT 3
 ALL4_CARMA STANDARD; PRT; 7 AA.
 ID ALL4_CARMA
 AC P81807;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 4.
 OS *Carcinus maenas* (Common shore crab) (Green crab).
 OC Bivalacustraca; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Subbrachyura; Portunoidea; Portunidae; Carcinus.
 NCBI_TaxID=6759;
 RN [1]
 RP SPECIENE.
 RC TISSUE=cerebral ganglion, and thoracic ganglion;
 RX MEDLINE=98121193; PubMed=941295;
 RA Dave H.; Johnsen A.H.; Maestro J.-L.; Scott A.G.; Jaros P.P.,
 Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Eur. J. Biochem. 250:727-734 (1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 KW -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 SEQUENCE 7 AA; 782 MW; 672879CDCB476AC0 CRC64;

Query Match 100.0% Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0; Indels 0; Gaps 0;
 Matches 0; Conservative 7; Mismatches 0; Delmiss 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 DPYAFGL 7

RESULT 4
 ALL5_CARMA STANDARD; PRT; 7 AA.
 ID ALL5_CARMA
 AC P81808;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 5.
 OS *Carcinus maenas* (Common shore crab) (Green crab).
 OC Bivalacustraca; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Subbrachyura; Portunoidea; Portunidae; Carcinus.
 NCBI_TaxID=6759;
 RP SEQUENCE.
 RC TISSUE=cerebral ganglion, and Thoracic ganglion;

RX MEDLINE=98121193; PubMed=941295;

RA Dave H.; Johnsen A.H.; Maestro J.-L.; Scott A.G.; Jaros P.P.,
 Thorpe A.;

RT "Isolation and identification of multiple neuropeptides of the

"allatostatin superfamily in the shore crab *Carcinus maenas*.";
 RL Bur. J. Biochem. 250:727-734 (1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 KW -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 Neuropeptide; Multigene family.
 SQ SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;

Query Match 100.0% Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0; Indels 0; Gaps 0;
 Matches 0; Conservative 7; Mismatches 0; Delmiss 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 NPYAFGL 7

RESULT 5
 ALL7_CYDPO STANDARD; PRT; 7 AA.
 ID ALL7_CYDPO
 AC P82158;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cydiastatin 7.
 OS *Cydia pomonella* (Codling moth).
 OC Bivalacustraca; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
 NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Dave H.; Johnson A.H.; Mastro J.-L.; Scott A.G.; Winsnaley D.,
 Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily";
 RL Peptides 18:1301-1308 (1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 SQ MOD RES 7
 SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;

Query Match 100.0% Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0; Indels 0; Gaps 0;
 Matches 0; Conservative 7; Mismatches 0; Delmiss 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 KNYDFGL 7

RESULT 6
 BRHP_CONIM STANDARD; PRT; 7 AA.
 ID BRHP_CONIM
 AC P58803;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bromopeptapeptide Im.
 OS *Conus imperialis* (Imperial cone).
 OC Bivalacustraca; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=3561;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

RC TISSUE=Venom;
 RX MEDLINE=97184108; PubMed=9030520;
 RA Craig A.G.; Jimenez B.C.; Dykert J.; Nielsen D.B.; Gulyas J.,
 Abogadie F.C.; Porter J.; Rivier J.E.; Cruz L.J.; Olivera B.M.,
 RA McInosh J.M.;
 RT "A novel post-translational modification involving bromination of

tryptophan. Identification of the residue, L-6-bromotryptophan, in peptide from *Conus imperialis* and *Conus radiatus* venom.";
 J. Biol. Chem. 272:4689-4698(1997).
 CC -: FUNCTION: Does not elicit gross behavioral symptoms when injected centrally or peripherally in mice.
 CC -: SUBCELLULAR LOCATION: Secreted.
 CC -: TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -: MASS SPECTROMETRY: MW=53.19; METHOD=ASIMS.
 DR PIR: A58112; AS8112.
 KW Bromination; Amidation; Pyrrolidone carboxylic acid.
 FT DISULFID 2 7 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 1 1 BROMINATION.
 FT MOD RES 6 6 AMIDATION.
 SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6DB7EA6B0 CRC64;
 Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 XXXXXX 7
 Db 1 QCGQAWC 7

RESULT 7
 CAPP_MYTED STANDARD; PRT; 7 AA.
 ID_CAPP_MYTED
 AC P1020;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1999 (Rel. 10, Last sequence update)
 DT 01-MAR-1989 (Rel. 10, Last annotation update)
 DE Catch-relaxing Peptide (CAPP).
 OS Mytilus edulis (Blue mussel).
 OC Bivalvia; Mollusca; Bivalvia; Pteriomorphia; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus;
 RN [1]
 RP SEQUENCE.

RA MEDLINE-8805022; PubMed=3576797;
 RA Hirata T., Kubota I., Kawahara A., Shimamoto N.,
 RA Muneoka Y.,
 RT "Catch-relaxing Peptide isolated from *Mytilus* pedal ganglia.";
 RL Brain Res. 422:374-376(1987).
 CC -: FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
 CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
 CC RETRACTOR MUSCLE.
 DR PIR: A28342; ECMURP.

FT MOD RES 7 7 AMIDATION.

SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7

Db 1 AMPMLRL 7

RESULT 8
 SEQUENCE. RX
 MEDLINE-89008313; PubMed=3139658;
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
 RA Adsit J.C., Dunn G.M., Suzuki A.;
 RT "Structure of CCP10, a peptide sex pheromone which induces
 conjugative transfer of the *Streptococcus faecalis* tetracycline
 resistance plasmid, CCP10.";
 RT RL J. Biol. Chem. 263:14514-14578(1988).
 CC -: FUNCTION: CCP10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC PLASMID PCF10.
 DR PIR; A30812; A30812.
 KW Pheromone.
 SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7

Db 1 LIVIIVFV 7

RESULT 9
 CHOX_ALCSP STANDARD; PRT; 7 AA.
 ID CHOX_ALCSP
 AC P16701;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE Choline oxidase (EC 1.1.3.17) (Fragment).
 OS Alcaligenes sp.
 OC Bacteriia; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Alcaligenes.
 OC NCBI_TaxID=512;
 RN [1]
 RP SEQUENCE.

RA MEDLINE-81006769; PubMed=62997283;
 RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
 RT "Identification and properties of the prosthetic group of choline
 oxidase from Alcaligenes sp.";
 RL J. Biochem. 88:197-203(1980).
 CC -: CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
 DR PIR: A15398; A15398.
 KW Oxidoreductase.
 FT NON TER 7 7
 SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7

Db 1 DNPNHSR 7

RESULT 10
 CIA_ENTPA STANDARD; PRT; 7 AA.
 ID CIA_ENTPA
 AC P11332;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CAM73 (Clumping-inducing agent) (CIA).
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteriia; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OC NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.

RA MEDLINE-87005252; PubMed=3093276;
 RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Suzuki A.,
 RA White B.A., An F.Y., Clewell D.B., Kitada C.,
 RN [1]

"Isolation and structure of the *Streptococcus faecalis* sex pheromone, CAM373.";
PT RT

RL RT "API, a sequenced bioactive neuropeptide isolated from the nematode
Neuron 2:1465-1473 (1989)."
CC -!- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTORNEURONS. REDUCES THE
INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE
CELLS.

CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFamide RELATED PEPTIDE)
FAMILY.

DR XW DR "A26269; A25289.
KW Pheromone.
SEQUENCE 7 AA: 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
Db 1 AIFLAS 7

RESULT 11
BIOS_LITRU

ID E105_LITRU STANDARD; PRT; 7 AA.

AC P82101;

DT 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Electron 5.

OS Litoria rubella (Desert tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;

OC Peleodidae; Litoria.

NCBI_TaxID:104895;

RN 11
RP TISSUE:Skin secretion

RA Wabnitz, P.A.; Bowie, J.H.; Tyler, M.J.; Wallace, J.C.; Wallace, J.C.;

RT Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from *Litoria*
litoria.",

RT Aust. J. Chem. 52:639-645 (1999).

RL CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- AMPHIBIAN defense peptide; Amidation.

KW MOD RES 7 7 AMIDATION

SEQUENCE 7 AA: 834 MW; 6DD05B076B05030 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XXXXXX 7
Db 1 TYPEPIA 7

RESULT 12
FARI_ASCSU

ID FARI_ASCSU STANDARD; PRT; 7 AA.

AC P31883;

DT 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DB FMRFamide-like neuropeptide API.

OS Eukaryota; Metazoa; Nematoidea; Ascaridoidea;

OC Ascaridida; Ascaris.

NCBI_TaxID:6253;

SEQUENCE 90180465; PubMed=2622777;

RX MEDLINE=90180465; PubMed=2622777;

RA Cowden C., Stretton A.O.W., Davis R.E.;

RESULT 13
FARI_HELT1

ID FARI_HELT1 STANDARD; PRT; 7 AA.

AC P41871;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DB FMRFamide-like neuropeptide GDPFLRF-amide.

OS Helisoma trivolvis (Snail).

OC Lymnaeoidea; Mollusca; Gastropoda; Pulmonata; Basommatophora;

OC NCBITaxID=27815;

RN [1] _RP SEQUENCES.

RT TISSUE=Kidney;

RT RX MEDLINE=94286117; PubMed=7912428;

RT RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;

RT trivolvis";

RT Peptides 15:31-36 (1994).

RL CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
THE KIDNEY, MANTLE AND SKIN.

CC CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.

CC CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFamide RELATED PEPTIDE)
FAMILY.

KW Neuropeptide; Amidation.

MOD RES 7 7 AMIDATION

SEQUENCE 7 AA: 851 MW; 69D4029D75AA810 CRC64;

Qy 1 XXXXXX 7
Db 1 GDPFLRF 7

RESULT 14
FARI_MACRS

ID FARI_MACRS STANDARD; PRT; 7 AA.

AC P83274;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DB FMRFamide-like neuropeptide FLPL (DGNFLRF-amide).

OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Bivalvia; Decapoda; Pleococemata; Caridea;

OC Palaeomonoidea; Palaeomidae; Macrobrachium.

OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE_Eyestalk;
 RA Sithigirngul P.; Saraiithongkum W.; Jaideechoey S.; Longyant S.;
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
 freshwater prawn Macrobrachium rosenbergii.",
 RT Comp. Biochem. Physiol. 120B:587-595 (1998).
 CC -!- MASS SPECTROMETRY; MN=965.7; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 967 MW; 69D0729C454OAC0 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Prod. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 XXXXXX 7
 :::::::
 Db 1 DRNFLRF 7

RESULT 15

PAR1 PROC1 STANDARD; PRT; 7 AA.
 ID PAR1 PROC1 STANDARD; PRT; 7 AA.
 AC P28499;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Cardiorexcitatory FMRFamide homolog NP1.
 OS Procambarus clarkii (Red swamp crayfish).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Bivalacostraca; Bivalvia; Decapoda; Pleocyemata; Astacidea;
 OC Astacidae; Cambiaridae; Procambarus.
 OX NCBI_TaxID=6728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE_Pericardial organs;
 RA Mercier A.J.; Orchard I.; Tebrugge V.; Skerrett M.;
 RT "Isolation of two FMRFamide-related peptides from crayfish
 pericardial organs.",
 RT Peptides 14:137-143 (1993).
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
 CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
 EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 7;
 Best Local Similarity 0.0%; Prod. No. 0;
 Matches 0; Conservative 7; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 XXXXXX 7
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 Db 1 NRNFLRF 7